

Minimising Take-all

Richard Gutteridge
Kim Hammond-Kosack



WGIN MM@NIAB
25th June 2009

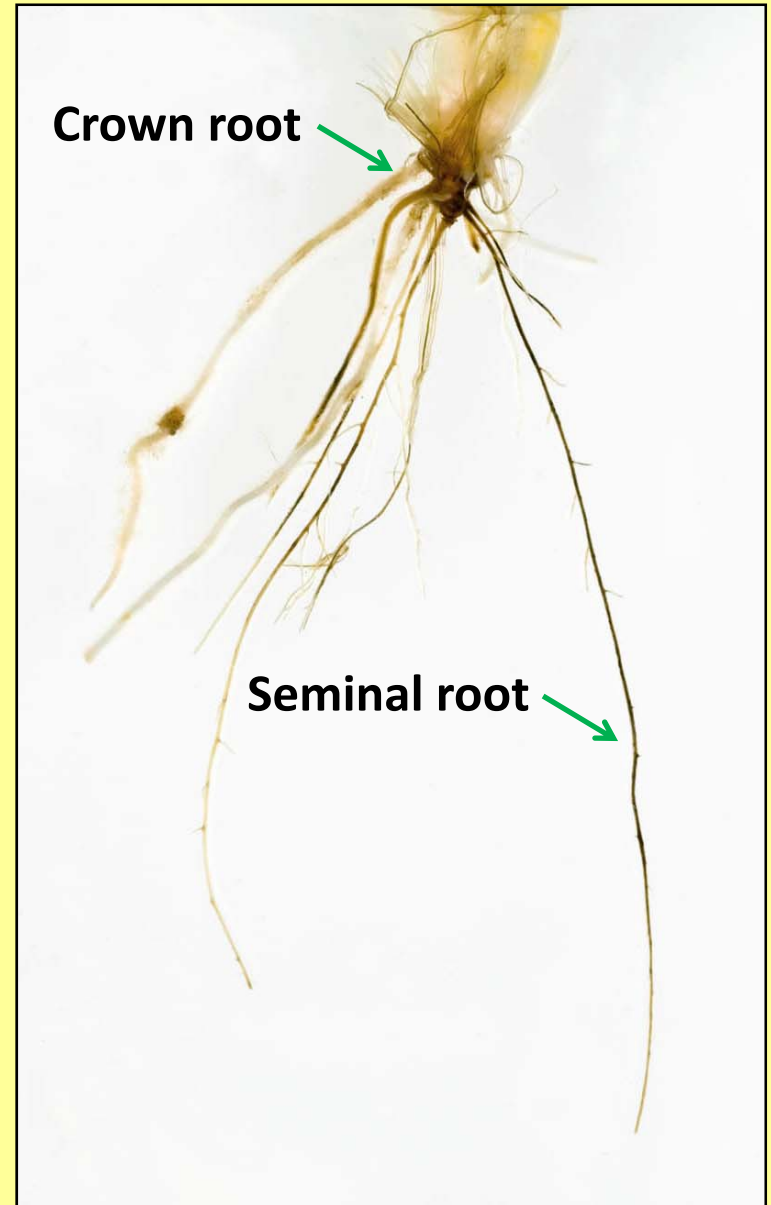
Take-all disease of wheat

- *Gaeumannomyces graminis* var. *tritici* (Ggt)

- ascomycete soil borne fungus

- related to rice blast fungus

Magnaporthe oryzae (previously *M. grisea*)



Ggt infected wheat seedling

A *Ggt* infected seminal root

Take-all lesion

Runner hypha



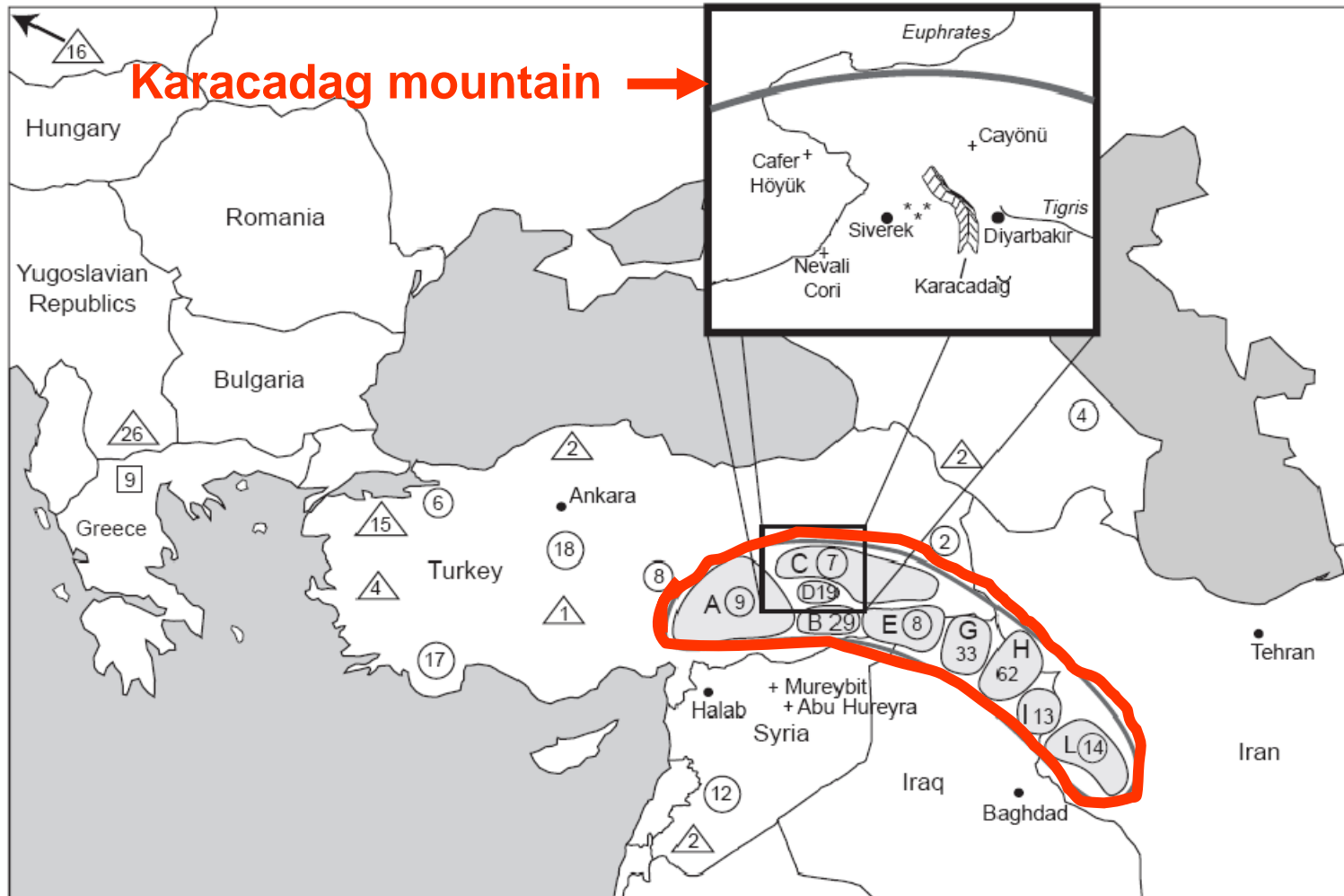


Typical take-all patch showing stunting and premature ripening of the crop

Talk Outline

- **Diploid wheat**
 - phenotyping via pot bioassay and field trials
 - mapping populations
- **Hexaploid wheat – Watkins / Gediflux collections**
 - field evaluations
 - results so far / future plans
- **Hexaploid wheat – inoculum build-up in 1st wheats**

T. monococcum domesticated from *T. boeoticum*



— Limits of Fertile Crescent

* Sampling of Karacadağ lines

+ Archeological site

○ *T. m. boeoticum*

△ *T. m. monococcum*

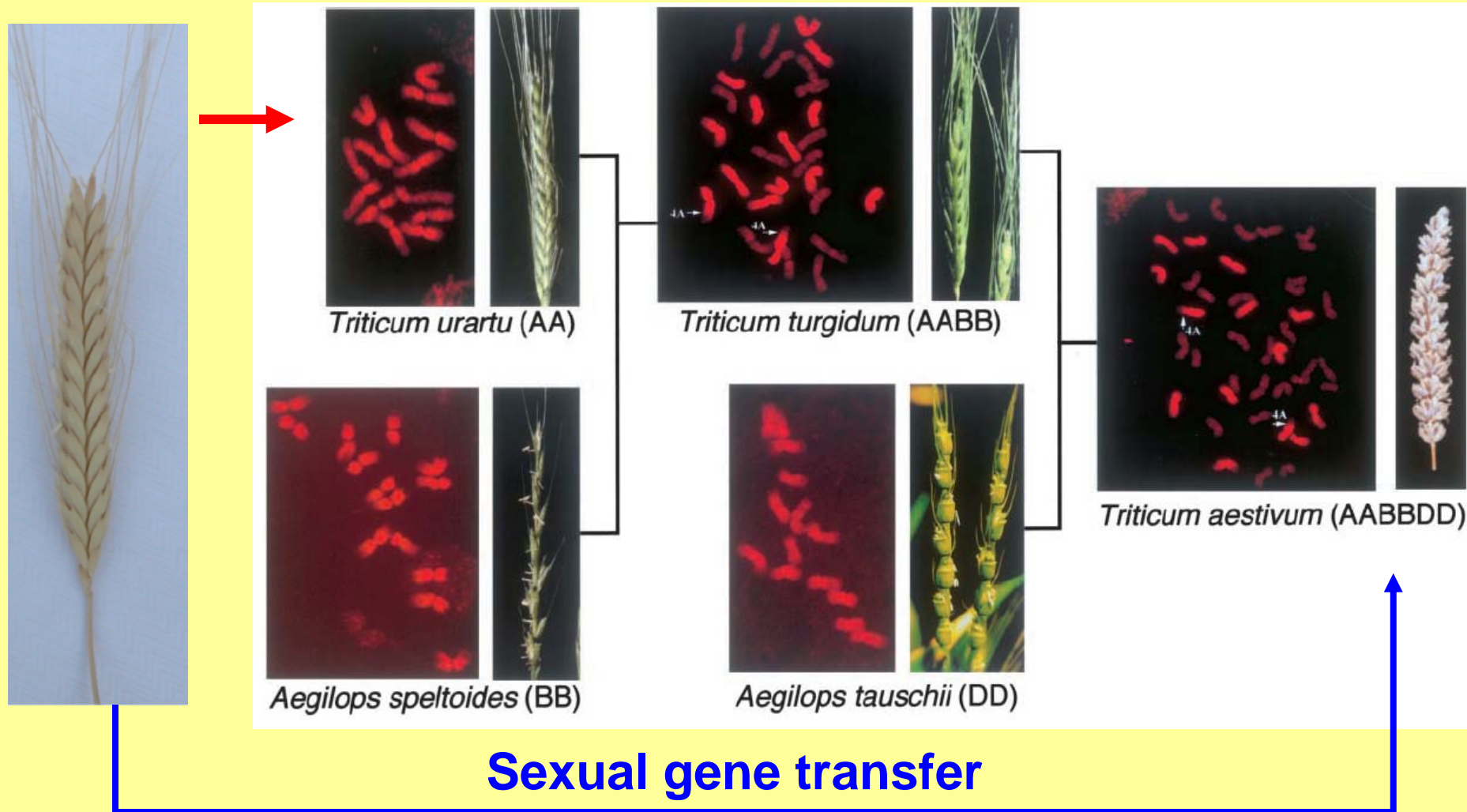
□ *T. m. aegilopoides*

(with number of samples)

A–L: areas of wild *T. m. boeoticum* sampling in the Fertile Crescent

Origin of bread wheat

T. monococcum A^mA^m

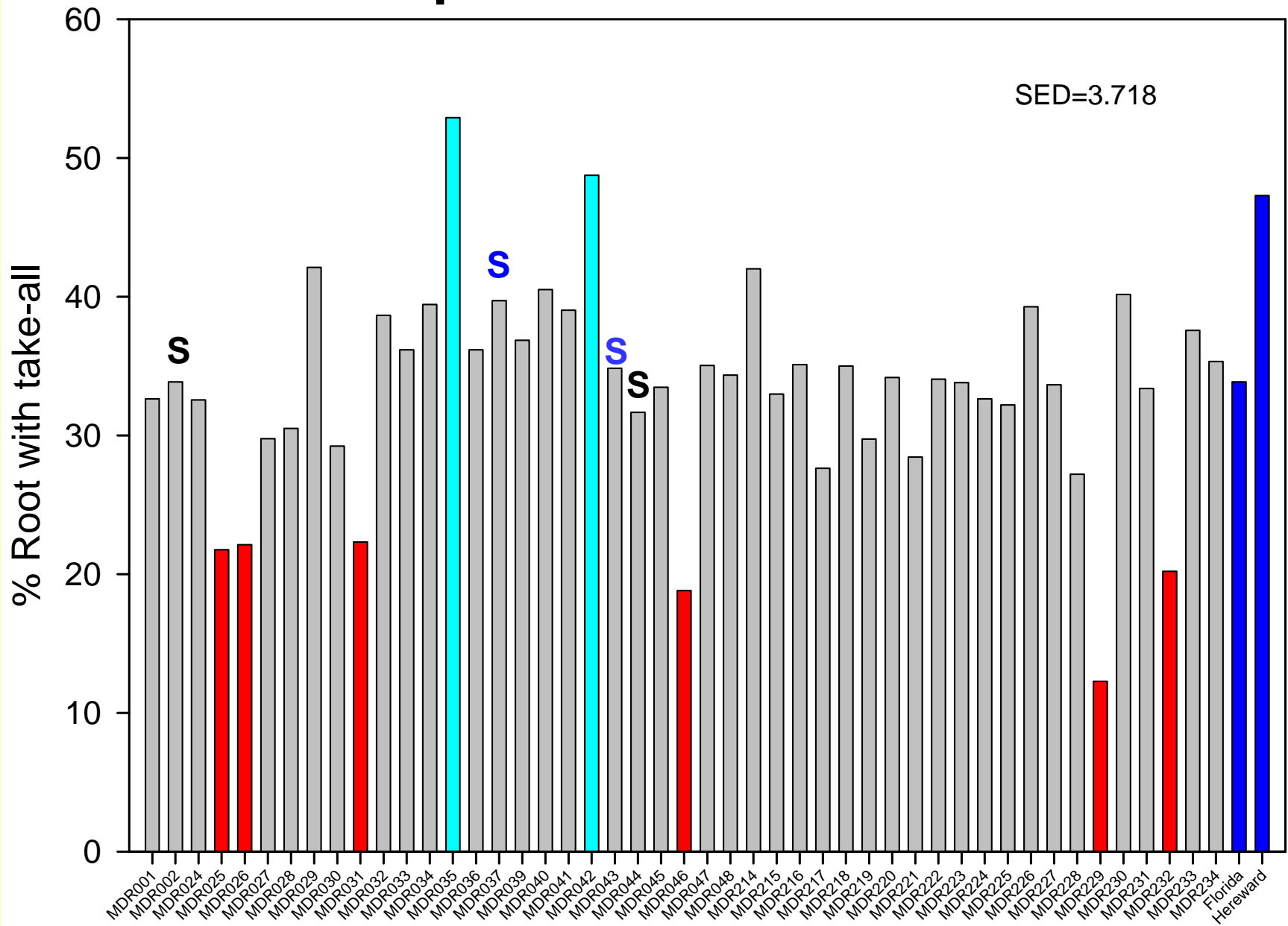


The Pot Take-all Bioassay – Two standard methods

- Collected field soil-crumble to an even texture, with large stones removed, stored in a cold room until required.
- Two experimental set-ups
 1. Fill pot fill with 50cc of moist sand, 300g of **naturally infected soil**, sown with 10 seeds evenly over the soil surface and covered with horticultural grit.
 2. **Artificial inoculum addition** - shake 300g of 'naïve' soil with 50g of dilute inoculum in a plastic bag, transfer to bioassay pot. (inoculum = sand/maize meal cultures, **10 different isolates**, including both A and B types, mixed together)

Min. 5 reps – total of 50 seeds

Pot exp 2007 – *T. monococcum*



Take-all Assessment of field experiments

Whole plant root systems are assessed in a white dish under water and the proportion of roots affected by the disease are graded as follows:

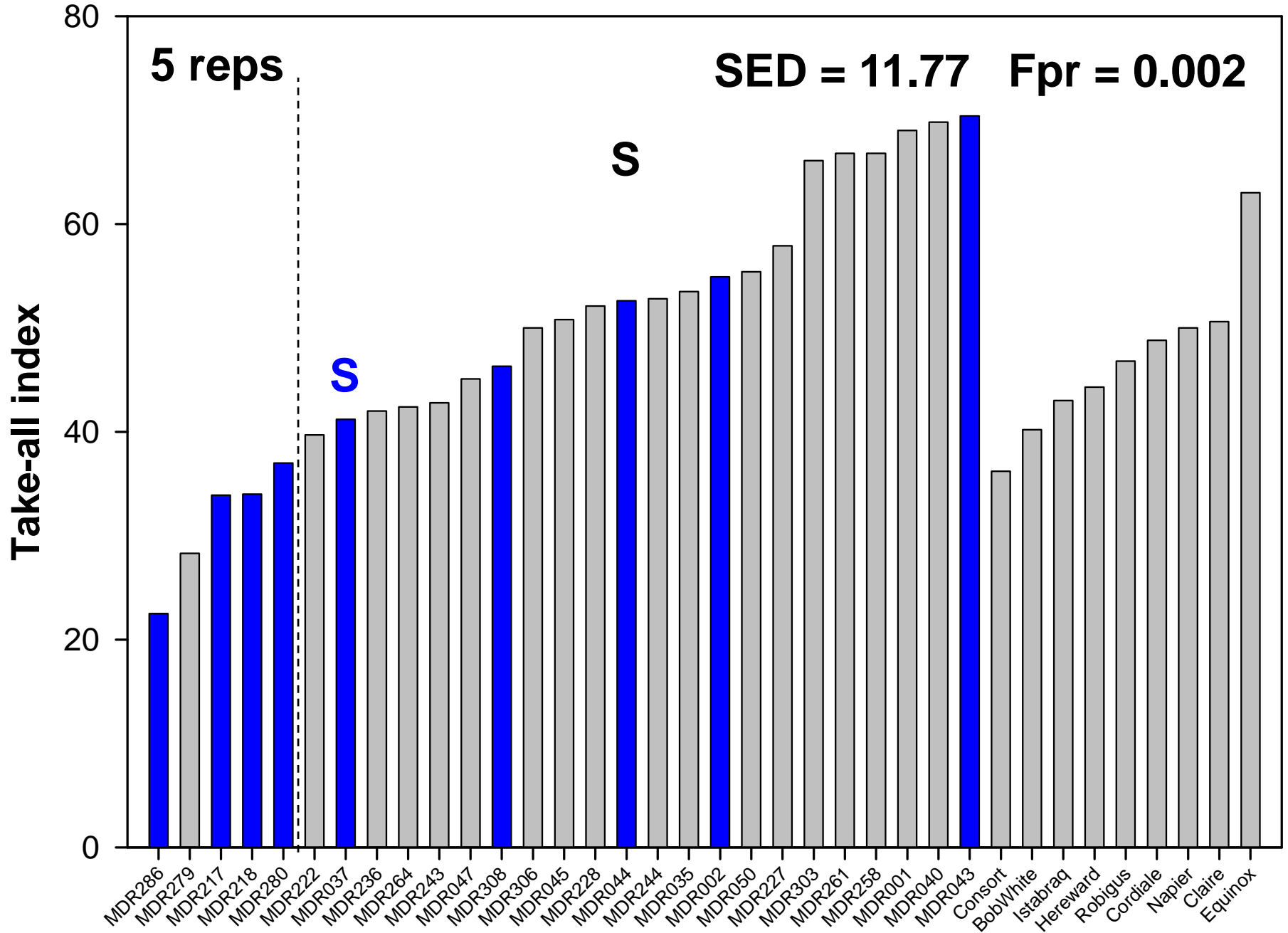
Slight 1: 1 – 12%; **Slight 2:** 13 – 25%; **Moderate 1:** 26 – 50%
Moderate 2: 51 – 75%; **Severe** >75%

Take-all Index (TAI) calculated by:

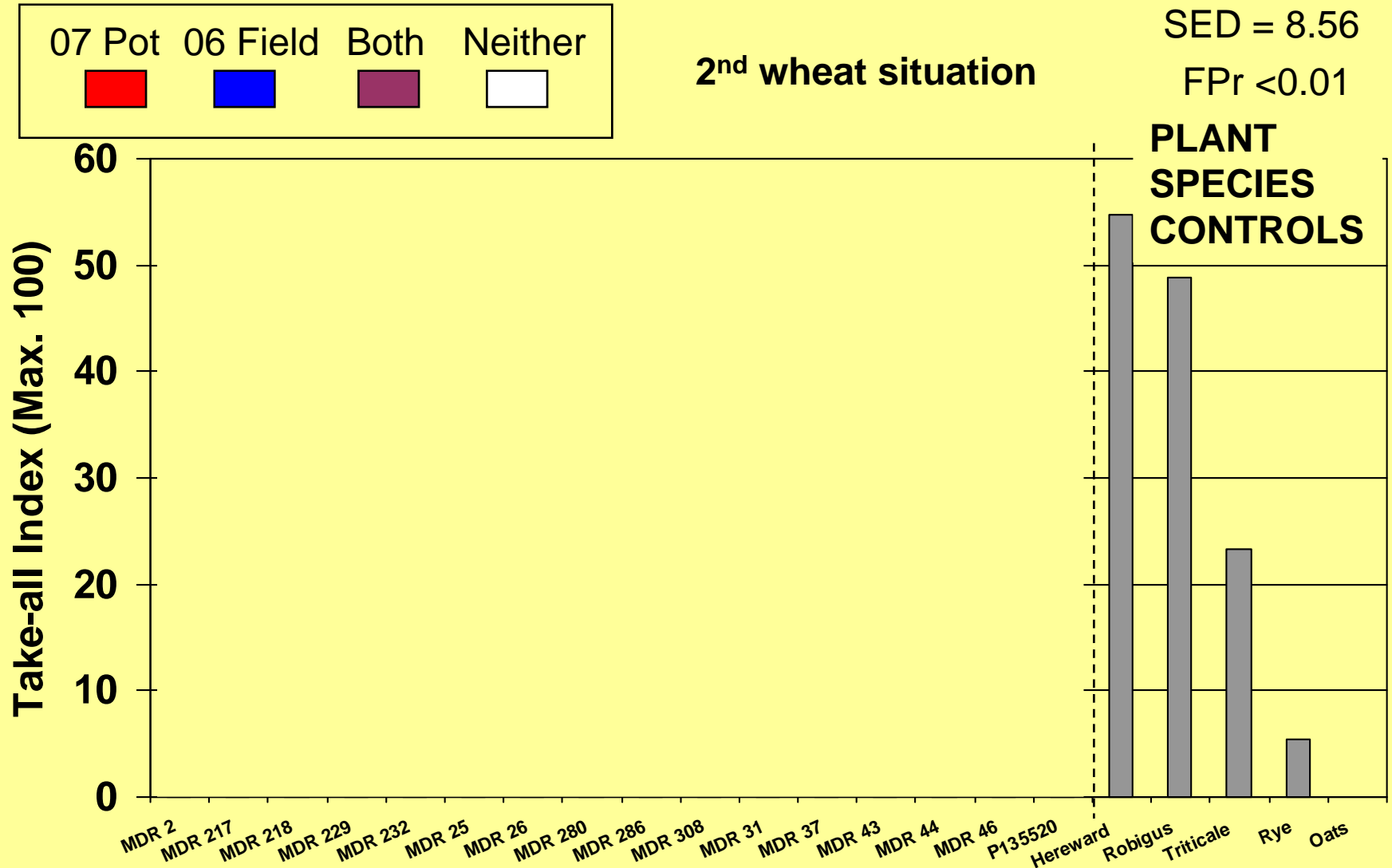
1 x %plants with slight 1; + 2 x %plants slight 2; + 3 x %plants moderate 1;
+ 4 x %plants moderate 2; + 5 x % plants severe

Divide by the number of categories (5) ; **Maximum index = 100**

Field experiment 2006 *T. monococcum* and *T. aestivum*

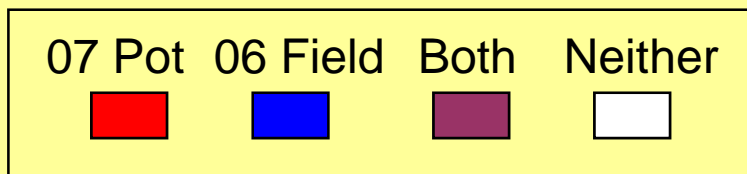


Field experiment 2008



5 rep exp but 10 reps MDR 37, MDR 46 and MDR 229

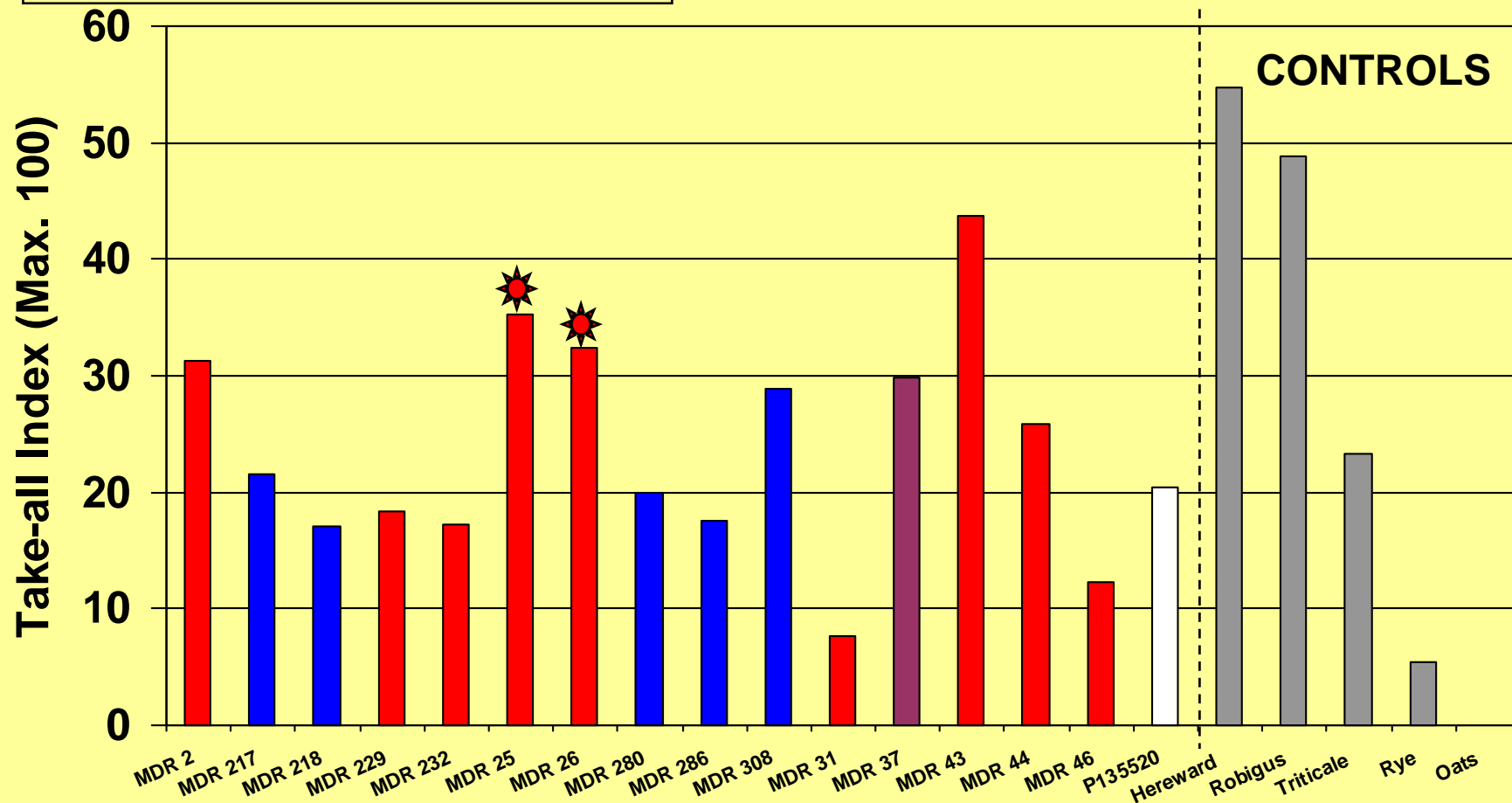
Field experiment 2008



2nd wheat situation

SED = 8.56

FPr < 0.01



5 rep exp but 10 reps MDR 37, MDR 46 and MDR 229

Summary of *T. monococcum* phenotyping results via pot bioassay and field (2006 – 2008)

Resistance leads

MDR 31

MDR 46

MDR 286

MDR 217

MDR 218

MDR 280

MDR 229

MDR 232

Highly susceptible genotypes

MDR 43, MDR 37, MDR 2, MDR 24, MDR 308 (DV92),
MDR 650 (P1355520)

- Genotypes used in an initial DArT marker analysis with a new Triticarte diploid wheat focussed array

Triticarte - custom wheat array

1536 clones derived from the two *T. monococcum* accessions

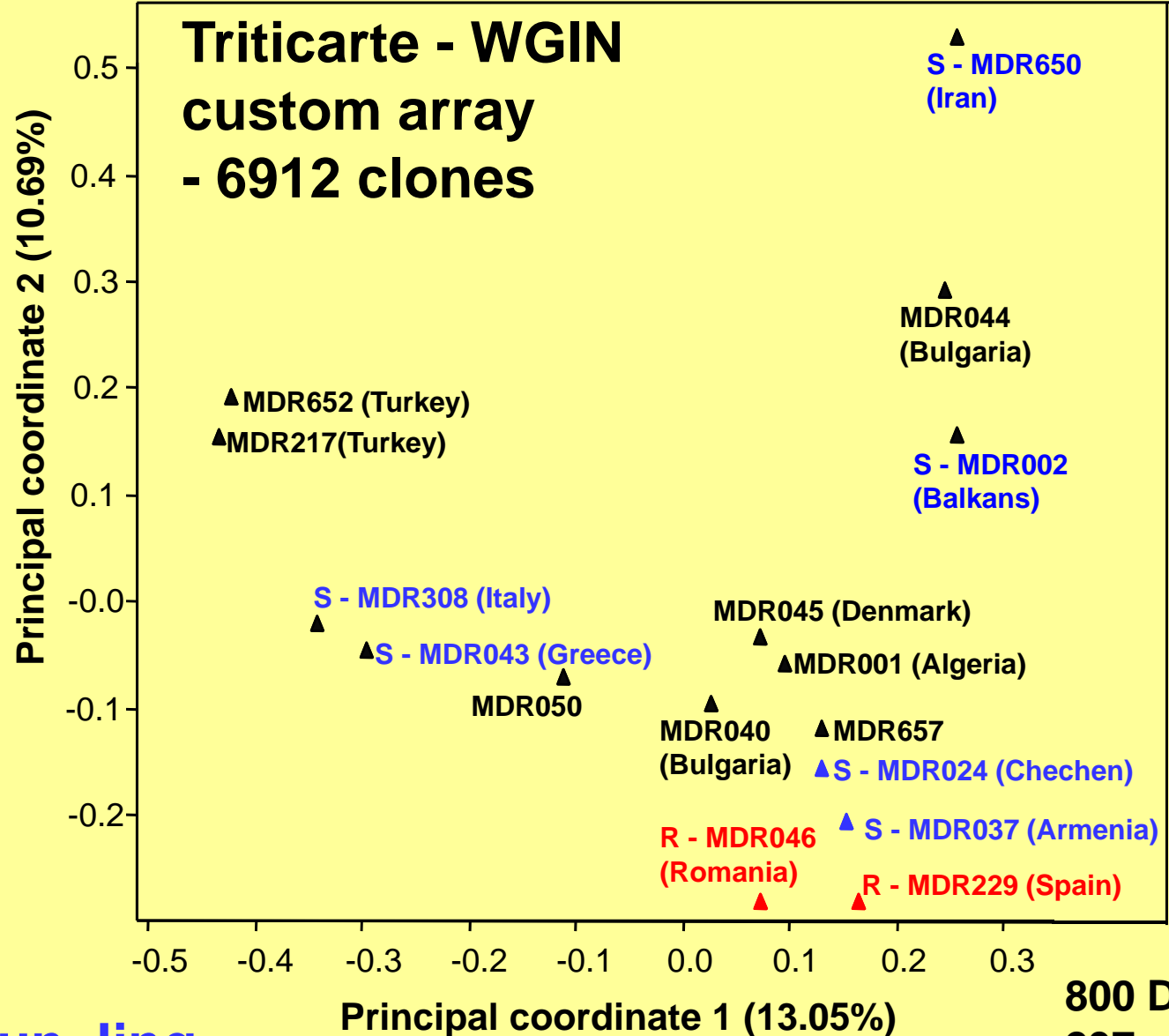
**2304 clones derived from hexaploid wheats
(including the Triticarte Wheat 2.3 array)**

**1536 clones derived from tetraploid durum wheat
(including the Triticarte Durum 2.0 array)**

**1536 clones derived from 15 Iranian accessions of
other *Triticum* species with genomes homologous
to the A-genome of bread wheat (Ali Mehrabi, unpublished)**

**Jing, Bayon, Kanyuka, Berry, Wenzl, Hunter, Kilian and Hammond-Kosack (2009)
Theoretical and Applied Genetics (under minor revision)**

DArT marker and PCA analysis of *T. monococcum* accessions



T. monococcum mapping populations

New crosses 2009

Resistant

MDR031

MDR046

MDR217

MDR229

Susceptible

MDR043

MDR037 - very early flowering, very tall

MDR002 – very late flowering

MDR308

MDR024

MDR650

T. monococcum mapping populations

Existing F₂ populations (sown 03-02-08)

MDR037 x MDR046 (R)

Awn colour / height

MDR037 x MDR229 (R)

Awn colour

Next steps

- To phenotype 100 F₃ lines using the pot bioassay
- To progress both populations to the F₆ generation using single seed descent, then re-phenotype (~300 lines for each popⁿ)

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The A. E. Watkins hexaploid wheat collection

Recently resurrected at JIC by Simon Orford within the WGIN project

1930's world wheat collection (local markets)

~ 740 accessions - genetically purified and sufficient seed available in Sept 2007

Full details - May 2008 WGIN Newsletter

Autumn 2007







The harvested roots – August 2008



root drying



**Stored at room temp prior
to assessment in a white tray
filled with water**



**severe
infection**



**light
infection**

Watkins Experiment 2008 RRes Take-all severity - control plots

Alpha design

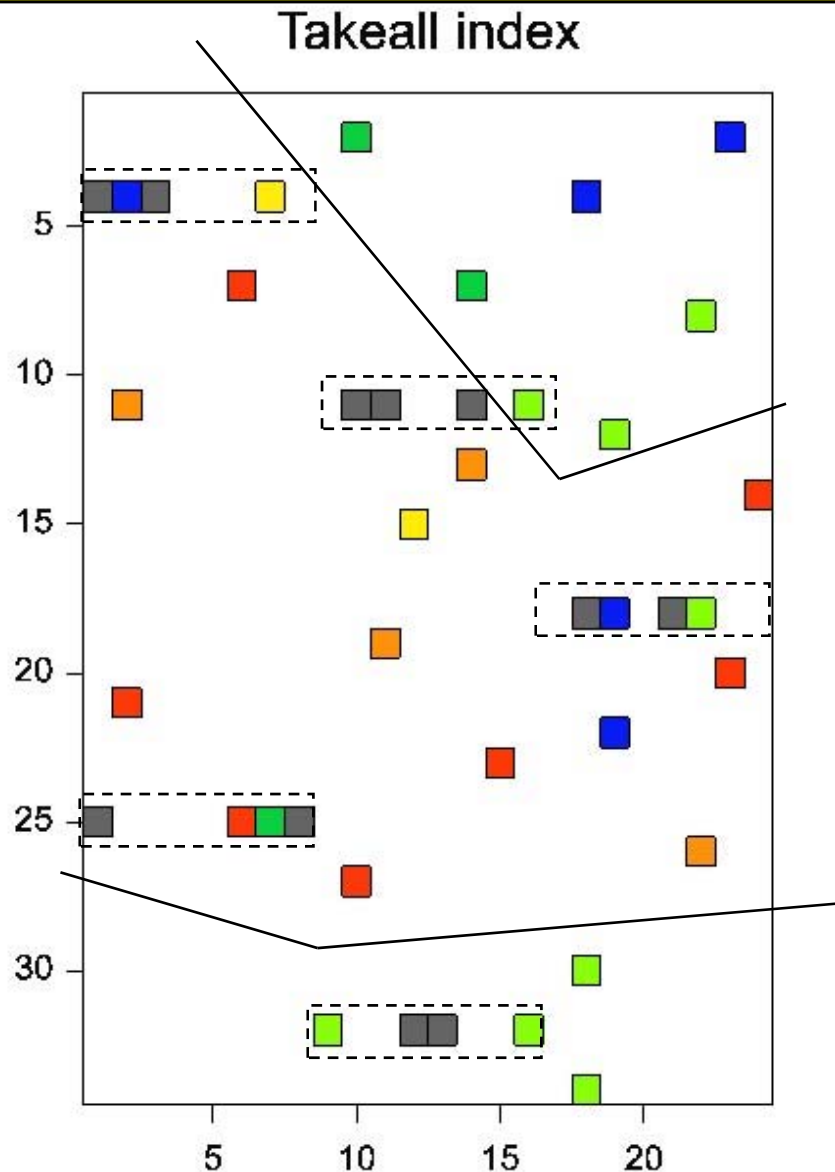
N = 800 plots

5 control blocks

Variety	TAI
Hereward	35.6
Triticale	18.4
Rye	1.7
Oats	0.0

TAI

Grey	0-5
Blue	6-15
Green	16-25
Light Green	26-35
Yellow	36-45
Orange	46-55
Red	> 55



Hereward - Extra 20 plots - mean TAI = 45.3

Mean of all plots
Hereward = 43.4

Watkins collection

2008 Take-all / eyespot assessments

- **Still to be assessed: 120 of the 740 lines**
- **Initial findings suggest that 226 lines (36%) can be omitted due to susceptibility to Take-all.**
- **A further 85 lines may also be discarded once the stats is completed**

A minimum of 309 lines to re-evaluate in trial year 2

Watkins collection – 2008 Eyespot assessment

Total number of straws	No. of straws with slight eyespot	No. of straws with moderate eyespot	No. of straws with severe eyespot
1677	661	432	361
% infected	39.4	25.8	21.5
% Total straws infected			86.7
% Straws with Moderate + severe infection			47.3

Table shows number of straws assessed for the hexaploid controls
(5 varieties x 5 replicates)

Number of Watkins lines to date showing moderate to good resistance to eyespot = 85 of 620 (14 %)

Watkins collection assessment 2008 - 2009

Identical experimental alpha design with the 740 lines

Third wheat situation – Take-all visible on roots since April

Fungicide treated for eyespot

- No eyespot assessments

**No assessment of the discarded Take-all susceptible lines
(at least 226 lines less)**

Assessing for floral diseases – in progress

Anticipated outcomes

Faster turn-a-round of the data

**A core of putative ‘resistant’ lines plus the ‘escapes’
due to the patchiness of disease development**

Disease escape lines present in the low Take-all patches

Alpha design

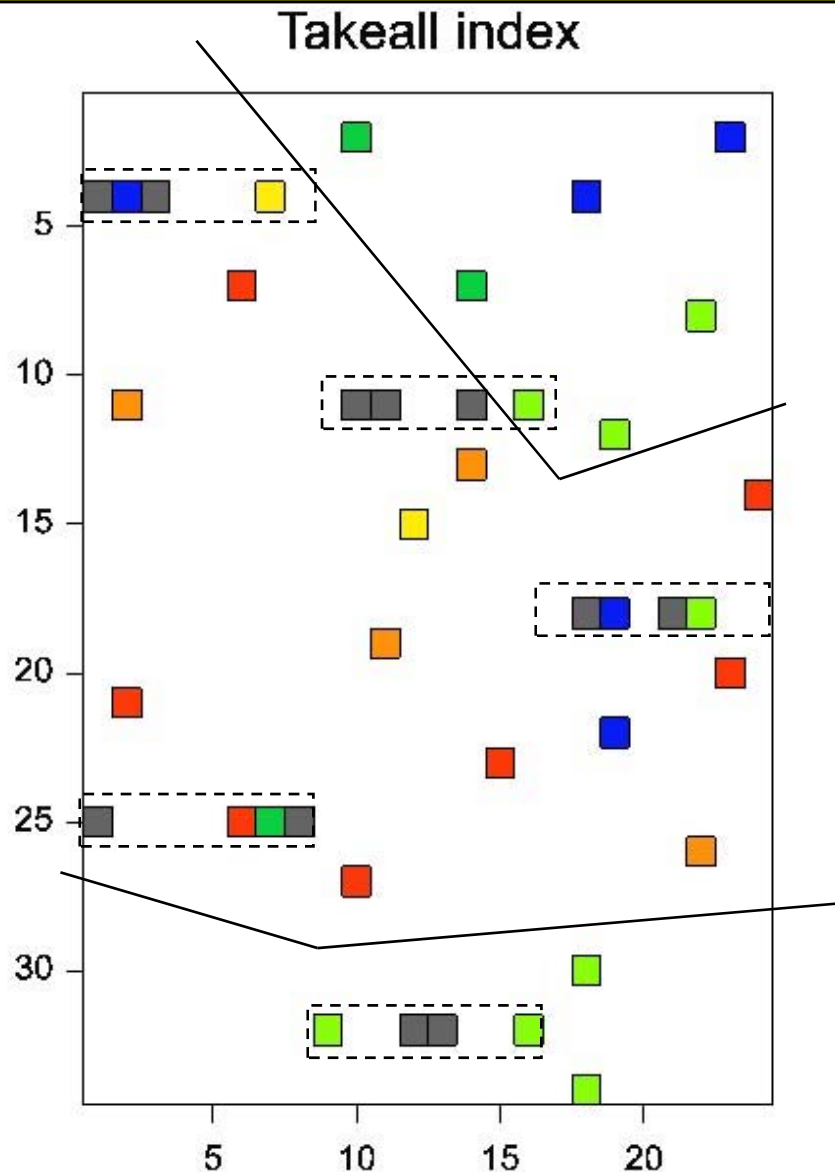
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Mean of all plots
Hereward = 43.4

Watkins / Gediflux collections assessment 2009 - 2010

Watkins

309 lines with promising results from the 2008 trial

X from 120 lines still to be assessed

Y from 85 lines – arising from the stats

Z new lines with seed now available (S. Orford)

~ 600 lines

Gediflux collection

Results Summary

- Soil pot bioassay can be used to identify likely sources of resistance/tolerance to take-all but inoculum concentration critical i.e. below 50% root infection.
- No evidence of new root proliferation associated with the low disease scores in either *T. monococcum* or *T. aestivum*
- *T. monococcum* resistance phenotypes benchmark between triticale and rye
- Association genetics in *T. monococcum* is giving promising results

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Take-all inoculum build-up

WGIN diversity trials – 1st wheats after oats

- **2004** onwards - WGIN trials - 200kg N plots only
 - Soil bioassay used to measure inoculum build-up
 - Range of hexaploid wheat varieties
 - Large plots 10 m x 3 m
 - 5 random cores per plot taken soon after harvest

1. Soil core taken angled underneath row



2. Core inverted into plastic cup



SOIL BIOASSAY

3. Ten wheat seeds (cv Hereward) sown



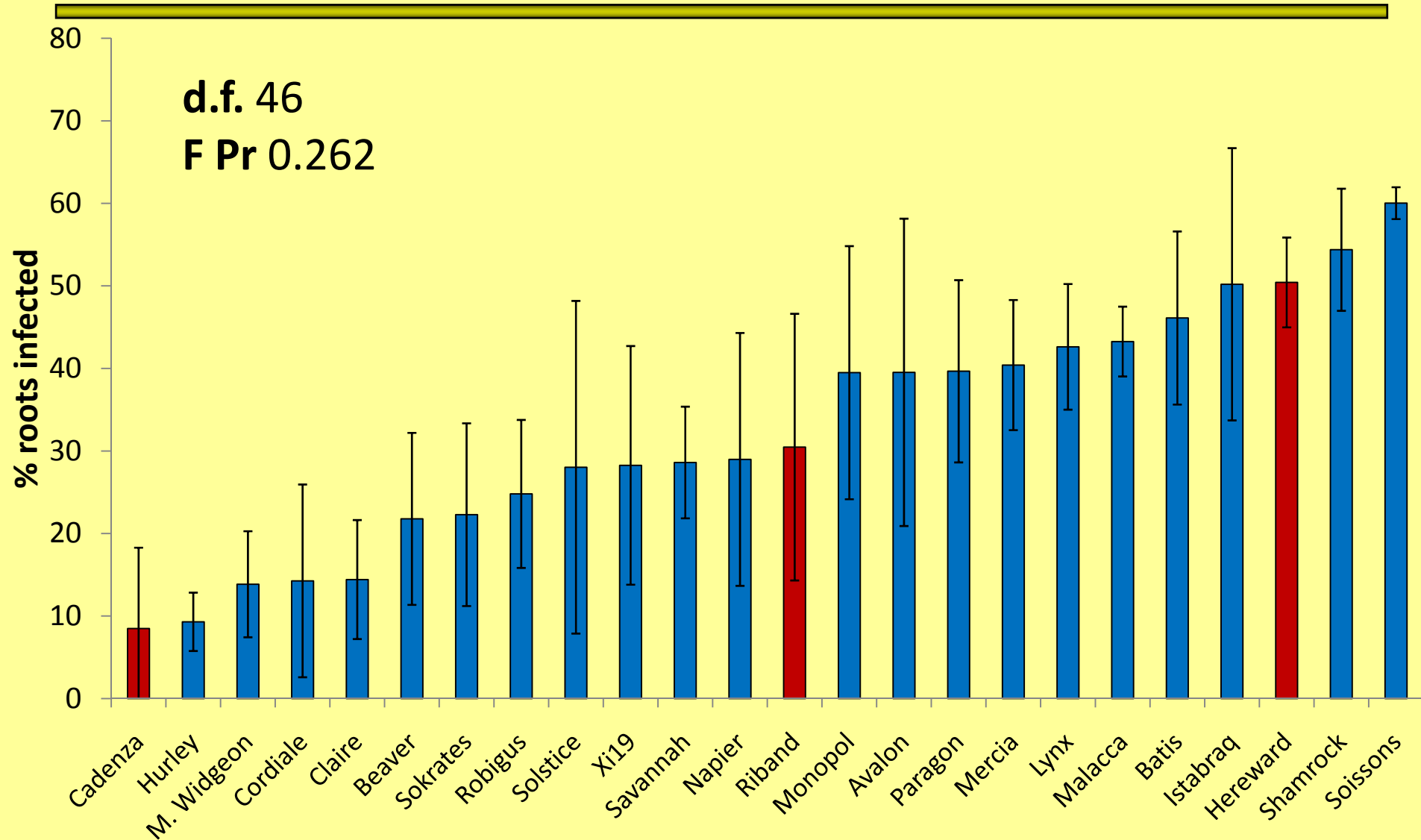
4. Growth room for 5 weeks



**Soil core
bioassay
plants**



Take-all infectivity of the soil after different winter wheat varieties (2008/R/WW/816)



Take-all infectivity of the soil

Variety	2004	2006	2007	2008	Overall ranking
Cadenza	1	2	1	1	1.25
Xi19	7	1	2	2	3
Riband	5	4	4	3	4
Mercia	3	5	3	6	4.25
Monopol	6	7	5	4	5.5
Avalon	2*	6	8	5	6.33
Soissons	8	3	6	9	6.5
Malacca	4	9	7	7	6.75
Hereward	9	8	9	8	8.5

1 = low 9 = high

SED= 0.781

Wald Statistic= 22.01

F pr= 0.009

The influence of wheat genotypes on Take-all inoculum build-up in 1st wheats

Immediate follow-up

1. Manuscript in preparation for Plant Pathology
2. Evaluating the new WGIN NUE diversity trial series
(2009 onwards)
3. Evaluating the entire Avalon x Cadenza DH mapping population
4. The new take-all inoculum build up (TAB) trial
(46 genotypes)

Many thanks to.....

Wheat Pathogenomics Team (RRes)

Richard Gutteridge
Sanja Treskic
Vanessa McMillan

Watkins Exp.
Simon Orford
Elke Anzinger

Hai-Chun Jing

The Triticarte team



BAB Dept
Statistics
Sue Welham
Rodger White



The Bioscience behind:



secure harvests

Global food security depends ultimately on growing enough crops. Economic, political and social factors are important, but sufficiency and sustainability of harvests are the primary needs.

The world's population is growing inexorably and harvests worldwide are threatened by climate change. Grain stores must be sufficient to protect against price volatility and speculation – particularly in poor, developing countries. Within a lifetime, regions near the equator could face agricultural losses of up to one-third.

We need to focus on where production gains are most readily and sustainably achievable. This means identifying and selecting crop traits and production systems that can increase yields in particular soils and climatic conditions, and reducing losses to pests and diseases. To do this requires knowledge of how

January 2009

WGIN 2008 Take-all *T. monococcum* trial

Increasing crop yields



Getting novel traits into wheat

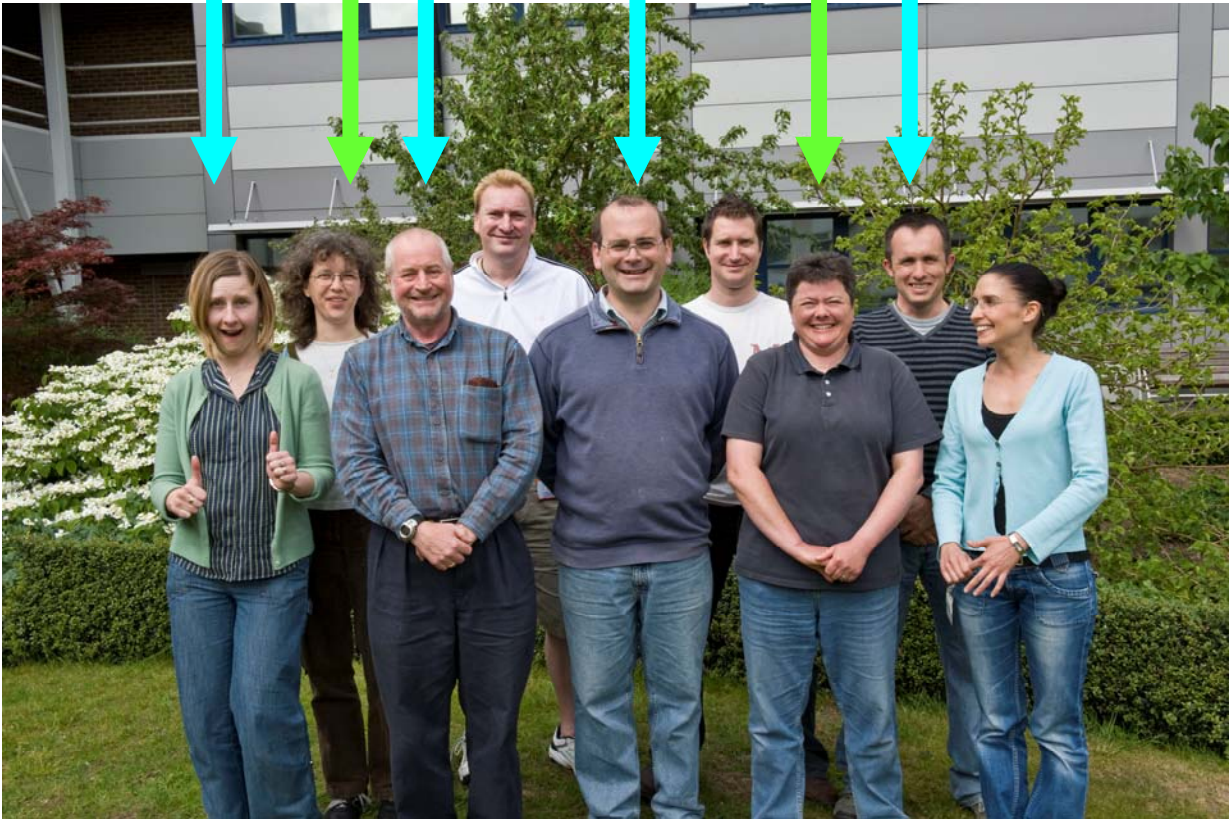
Some of wheat's wild relatives have potentially useful traits such as drought-tolerance and disease-resistance. But these cannot be bred into commercial varieties because of a mechanism in wheat that prevents its chromosomes from swapping genes, except with other wheat plants.

Scientists at the JIC have found that a gene called *Ph1* senses when parental wheat chromosomes match and allows them to cross. They are identifying ways to block *Ph1* temporarily so that breeders can cross wheat varieties with wild relatives to obtain hybrids with new traits. Once a useful gene is incorporated, *Ph1* would be switched on again, fixing the new gene in subsequent generations of the crop.^[6]

JIC WGIN 2 Team

Michelle Leverington
Luzie Wingen
John Snape

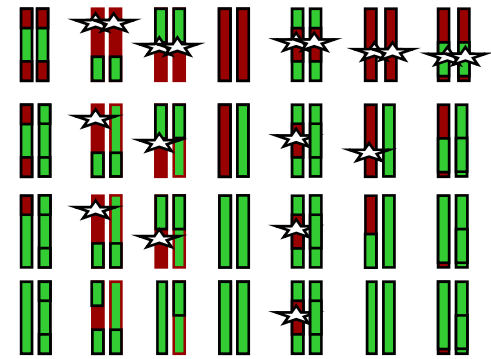
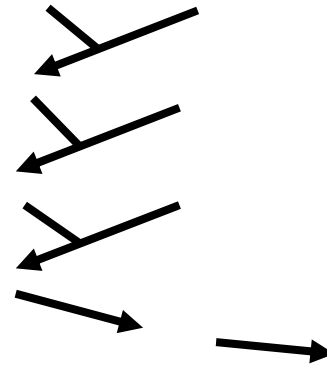
Simon Griffiths
Lesley Fish
Simon Orford



Development of Near Isogenic Lines

Near Isogenic Line development

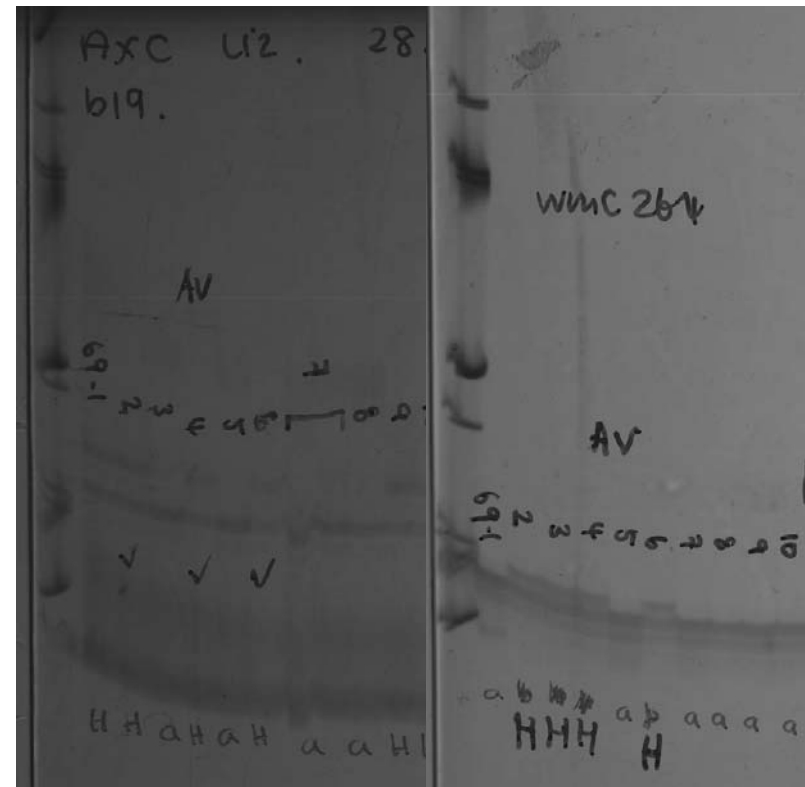
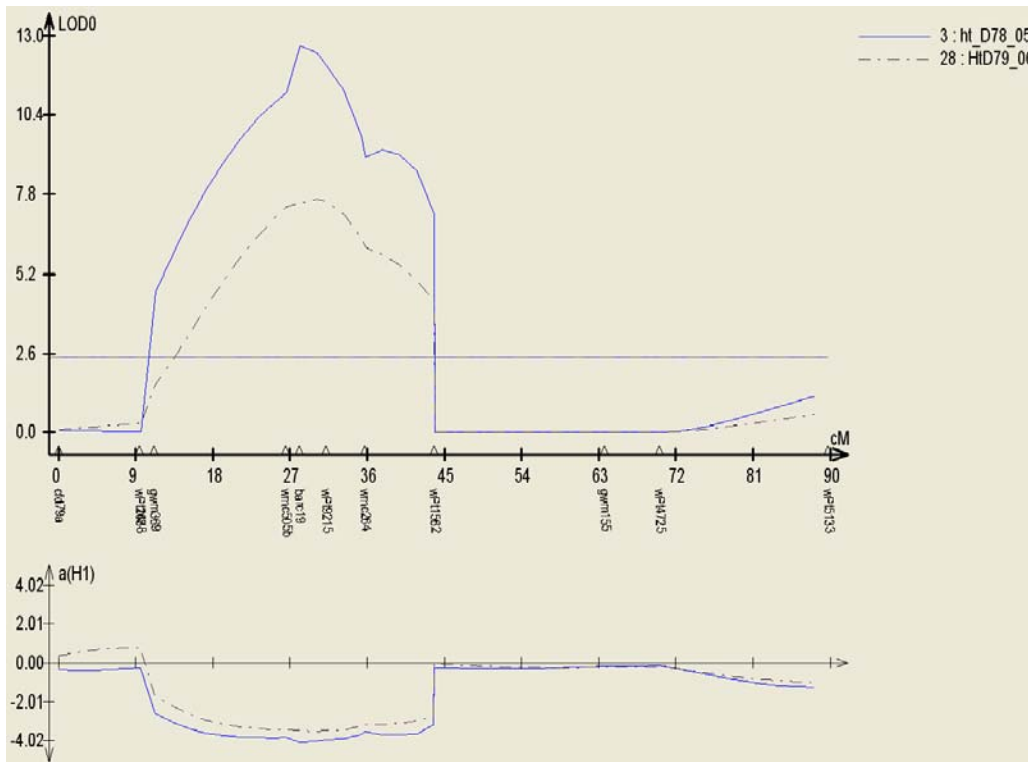
-Example of strategy for 3A height



WGIN1



WGIN2



Near isogenic line development- Yield

QTL	F ₁	BC ₁	BC ₂	Homozygotes
2D				
3B				
5A				
7B				
7D				

Near isogenic line development- Crop height

QTL	F ₁	BC ₁	BC ₂	Homozygotes
2A	Dark Blue	Dark Blue	Dark Blue	White
2D	Dark Blue	Dark Blue	Diagonal Hatching	White
3A	Dark Blue	Dark Blue	Dark Blue	Dark Blue
3B	Dark Blue	Dark Blue	Diagonal Hatching	White
6A	Dark Blue	Dark Blue	Dark Blue	White
6B	Dark Blue	Dark Blue	Dark Blue	White

Near isogenic line development- Ear emergence

QTL	F ₁	BC ₁	BC ₂	Homozygotes
1B				
1D				
6B				

Gamma mutagenesis

"And he gave it for his opinion, that whosoever could make **two ears of corn** or two blades of grass to grow upon a spot of ground where only one grew before, would deserve better of mankind, and do more essential service to his country, than the whole race of politicians put together."

— [Jonathan Swift](#) ([Gulliver's Travels](#))



Gamma M2 mutants: CS left
Paragon right
Frequent flag leaf rolling



Gamma M2 mutants:
CS bagged left (2500 sown). Paragon (2000 sown) currently bagging right
50% fertility rate expected

Taking Paragon EMS alleles
forward

Tagging plants by visiting students for
DNA collection and trait scoring



Leaf senescence seg



Mutant x Spring cultivars: F2 families

12 families – segregations of mutant types height, flowering, leaf senescence
and biomass



Paragon mutants in Hege 80s

Left – flowering time differences (first two plots) Right – leaf senescence

Populations

Ten AE Watkins x Paragon SSD populations- now at F_3

- Extremes- height and ear emergence
- More to come eg- Thousand grain weight, grain length and grain width measured on 1100 Watkins lines
- Also 2 SSDs Paragon X CS and JIC synthetic up to F_4 .

Avalon x Cadenza workshop

- When 29th Oct or 5th Nov
- Where?
- JIC continues to maintain stocks

Handling data

- Development of relational database as core resource at JIC
- Propose to link version containing WGIN data to WGIN website



Navigation

- Home
- Browse Accession Data
- Map Data
- Group Data
- Trial Data
- Phenotype Data

General Options

- About This Database
- Credits

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To view markers contained on a map choose a map from the table below and click on its description.

Description	Created On	Updated On
JIC 2007 Savannah X Rialto map (SaXRi or RxS)	2009-05-28 16:47:21	
JIC 2007 Malacca X Charger map (MaXCh or MxC)	2009-05-28 17:10:00	
JIC 2006 Charger X Badger map (ChXBa or CxB)	2009-05-28 17:13:48	
JIC 2006 Beaver X Soisson map (BeXSo or BxS)	2009-05-28 17:31:43	
JIC 2009 Avalon X Cadenza map (AvXCa or AxC)	2009-05-28 17:43:59	

[Back](#)



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- Home
- Download Accession Data
- Map Data
- Group Data
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- Genotype Data

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- About This Database
- Help

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JIC 2006 Beaver X Soisson map (BeXSo or BxS)	2009-05-28 17:31:43	
JIC 2009 Avalon X Cadenza map (AvXCa or AxC)	2009-05-28 17:43:59	

Retrieving map data for map : JIC 2009 Avalon X Cadenza map (AvXCa or AxC)

The table below contains further information about markers contained on your selected map. Clicking the marker name will take you to further information about that particular marker while clicking the 'MapChart Format' button will allow you to export the map in MapChart format. For further information about MapChart please visit <http://www.biometris.wur.nl/uk/Software/MapChart/>

[Export to MapChart Format](#)

Show Marker Data

Marker Name	Close Index	Map Feature Description	Chromosome	Feature Start	Feature End
Tagluten	1A	Gene	1A	0.00	0.00
wmc336a	1AS	SSR	1A	3.00	3.00
I102W1		Gene	1A	4.00	4.00
psp3027	1A	SSR	1A	6.00	6.00
gwm164	1A	SSR	1A	7.00	7.00
gwm498	1A	SSR	1A	8.00	8.00
GluA1		Gene	1A	9.00	9.00
wPt9757		DArT	1A	10.00	10.00
wmc93		SSR	1A	11.00	11.00
gwm99	1A	SSR	1A	12.00	12.00
gwm33a	1B	SSR	1B	0.00	0.00
wPt2230	1BS	DArT	1B	1.00	1.00
TaglgapG	1BS	Gene	1B	2.00	2.00
gwm264	5A	SSR	1B	3.00	3.00



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- Browse Accession Data
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- Group Data
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Categorical Data Export

From these pages you are able to view phenotypic data that is held by Germinate...

[Go to the Chart Utility](#)

Experiment Name	Description	Date
JIC NUE 2008 Savannah X Rialto DH phenotypes	JIC SaXRi DH phenotypes from field trial in Bawburgh, 2008, at two nitrogen levels (low n and nor n). (Population also wrongly called RiXSa)	2007-10-16
JIC 2007 Avalon X Cadenza DH phenotypes	JIC AvXCa DH phenotypes from field trials in Bawburgh for WGIN project, 2007	2006-10-01

[Back](#)

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Dataset Description	Dataset Date	Version	Experiment Name
spikelet number per ear;2007			JIC 2007 Avalon X Cadenza DH phenotypes
ear length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
straw biomass;2007			JIC 2007 Avalon X Cadenza DH phenotypes
ear biomass;2007			JIC 2007 Avalon X Cadenza DH phenotypes
peduncle length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
internode1 length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
internode2 length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
internode3 length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
1000-dehulled grain weight;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes
grain surface area;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes
grain width;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes
grain length;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes

Ok we are looking at dataset 1000-dehulled grain weight;2007

This dataset has the following phenotypes defined against it.

Name	Short Name	Description	Export
1000-dehulled grain weight	TGRWT	The weight, measured in grams, of 1000 well-developed whole grains (without hull).	<input type="checkbox"/>

Submit

[Back](#)

- Home
- Browse Accession Data
- Map Data
- Group Data
- Trial Data
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- General Options
- About This Database
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New WGIN Website

www.wgin.org.uk



The screenshot shows the homepage of the WGIN website. At the top, there is a navigation bar with links for 'home', 'site map', and 'contact us'. The main header features the Defra logo on the left, the 'WGIN' acronym in large orange letters in the center, and the 'Wheat Genetic Improvement Network' logo on the right. Below the header is a horizontal menu with four categories: 'ABOUT', 'INFORMATION', 'RESOURCES', and 'STAKEHOLDERS'. The main content area is divided into two columns. The left column contains a welcome message for the 2009-2013 phase, a background section with a photograph of wheat, and a 'RECENT UPDATES' section. The right column contains a 'site guide' section with a list of site sections and their purposes. At the bottom, there is a footer with logos for Defra, Rothamsted Research, The University of Nottingham, and John Innes Centre, along with contact information and a 'Last updated: June 2009' note. The browser's taskbar at the bottom shows 'Local intranet' and '100%' zoom.

home | site map | contact us

defra
Department for Environment
Food and Rural Affairs

WGIN

monogram
Wheat
Genetic
Improvement
Network

ABOUT INFORMATION RESOURCES STAKEHOLDERS

HOME >

Welcome to WGIN 2nd Phase (2009-2013)

Defra Wheat Genetic Improvement Network - Improving the environmental footprint of farming through crop genetics and targeted traits analysis

Background

The UK government is committed to more sustainable agriculture but this vision is facing an ever expanding range of environmental, energy and climate change challenges. Wheat is grown on a larger area and is more valuable than any other arable crop in the UK. Established in 2003, the Wheat Genetic Improvement Network (WGIN) arose directly from a realisation in the early 2000s that over the preceding two decades there had been a widening disconnection between commercial plant breeding activities and publicly funded plant and crop research. The overall aim of WGIN is to generate pre-breeding material carrying novel traits for the UK breeding companies and to deliver accessible technologies, thereby ensuring the means are available to produce new, improved varieties. An integrated scientific 'core' which combines underpinning work on molecular markers, genetic and genomic research, together with novel trait identification, are being pursued to achieve this goal.



RECENT UPDATES
OLD Site - The old site is still available here.

site guide

The site is grouped into the following four sections:

- ABOUT** - for general information about WGIN, including news items and contacts.
- INFORMATION** - for more detailed information about WGIN, including reports and information tools.
- RESOURCES** - for experimental resources and research related tools
- STAKEHOLDERS** - for information on the Stakeholders Forum

Please use our interactive dropdown menus, the side menus, or the link tracker to navigate the site.
--see site-map for overview

Sponsored by: Defra (UK) 
Hosted by: Rothamsted Research 
Maintained by: Elke Anzinger 
Edited by: Kim Hammond-Kosack 
Designed by: Pierre Carion 
Last updated: June 2009

defra
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ROTHAMSTED
RESEARCH

Local intranet 100%

New WGIN Website

- Streamline format for easier navigation and information access
- Design is based on the OREGIN website, the design has kindly been provided by Pierre Carrion, web designer for OREGIN



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Defra Wheat Genetic Improvement Network - Improving the environmental footprint of farming through crop genetics and targeted traits analysis

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The UK government is committed to more sustainable agriculture but this vision is facing an ever expanding range of environmental, energy and climate change challenges. Wheat is grown on a larger area and is more valuable than any other arable crop in the UK. Established in 2003, the Wheat Genetic Improvement Network (WGIN) arose directly from a realisation in the early 2000s that over the preceding two decades there had been a widening disconnection between commercial plant breeding activities and publicly funded plant and crop research. The overall aim of WGIN is to generate pre-breeding material carrying novel traits for the UK breeding companies and to deliver accessible technologies, thereby ensuring the means are available to produce new, improved varieties. An integrated scientific 'core' which combines underpinning work on molecular markers, genetic and genomic research, together with novel trait identification, are being pursued to achieve this goal.



RECENT UPDATES

OLD Site - The old site is still available here.

site guide

The site is grouped into the following four sections:

ABOUT - for general information about WGIN, including news items and contacts.
INFORMATION - for more detailed information about WGIN, including reports and information tools.
RESOURCES - for experimental resources and research related tools
STAKEHOLDERS - for information on the Stakeholders Forum

Please use our interactive dropdown menus, the side menu, or the link tracker to navigate the site.
--see site-map for overview


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Hosted by: Rothamsted Research 
Maintained by: Elke Anzinger
Edited by: Kim Hammond-Kosack
Designed by: Pierre Carrion
Last updated: June 2009

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home | site map | contact us

OREGIN

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OREGIN

ABOUT INFORMATION RESOURCES STAKEHOLDERS

HOME >

Defra OILSEED RAPE GENETIC IMPROVEMENT NETWORK

Welcome to OREGIN

Providing a pre-breeding pipeline, to integrate sustainability traits into Oilseed Rape cultivars

The Oilseed Rape Genetic Improvement Network (OREGIN) has been successful in achieving initial objectives of providing a focus for the UK Oilseed Rape genetic improvement R&D and stakeholder communities, and a mechanism for prioritising research requirements. The principal activities of the OREGIN project are the generation, gathering, collation and dissemination of information and genetic resources for the benefit of the stakeholders. Ongoing discussions amongst the R&D and breeder communities have identified the highest priority requirements in the context of Defra strategic objectives. It is recognised that other trait areas such as pest resistance may be of increasing commercial priority and affect the long-term sustainability of the crop. The components of the OREGIN pre-breeding platform will also provide a foundation for and contribute significantly to other projects of relevance to the overall objectives of achieving improvements in sustainability through crop genetic improvement.



This new site has been divided into the following four sections:

- About - "What is OREGIN?", project outline, news, contact details and information on the other Defra crop genetic improvement networks

site guide

The site is grouped into the following four sections:

ABOUT - for general information about OREGIN, including news items and contacts.
INFORMATION - for more detailed information about OREGIN, including reports and information tools.
RESOURCES - for experimental resources and research related tools
STAKEHOLDERS - for information on the Stakeholders Forum

Please use our interactive dropdown menus, the side menu, or the link tracker to navigate the site.
--see site-map for overview

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Old WGIN Website



The screenshot shows the homepage of the Wheat Genetic Improvement Network (WGIN) website. The header features the Rothamsted Research logo, the WGIN title, and the Defra logo with supporting text. A navigation menu includes Home, Research Activities, Resources, and Stakeholders. The main content area has a search bar and a large graphic titled 'Delivery of genetic improvement in wheat- The role of UK science'. This graphic illustrates a process flow from 'Genetics' (Genetic analysis, Positional Cloning, Mutants) to 'Germplasm' (Collections, Mapping populations, Mutant populations) to 'Genomics' (Public), which then leads to 'Prioritising Targets- Breeders and Government' and finally to 'Processors' (UK agriculture, Rural livelihoods, Global agriculture, Biodiversity, Landscape). A 'Recent Additions' section is also visible.

Wheat Genetic Improvement Network

Initiated and supported by the Department for Environment, Food and Rural Affairs Part of the Defra Crop Genetic Improvement Networks

Home Research Activities Resources Stakeholders

Home

WGIN - a project supported by Defra

Search the WGIN site

Recent Additions

Delivery of genetic improvement in wheat- The role of UK science

- Genetics**
 - Genetic analysis
 - Positional Cloning
 - Mutants
- Germplasm**
 - Collections
 - Mapping populations
 - Mutant populations
- Genomics**
 - Public

Prioritising Targets- Breeders and Government

Processors

- UK agriculture
- Rural livelihoods
- Global agriculture
- Biodiversity
- Landscape

Printer friendly page [Site Map](#) Hosted by Rothamsted Research Maintained by Elke Anzinger Trevor Pocock Last updated: Wednesday, 24 June, 2009

Additional information on the new website

- Annual reports to Defra will be posted on the website
- Specific page for related projects
- Specific page for subcontractor projects
- Specific pages for datasets on mapping and markers
- GANTT charts and milestones for each research objective

Accessing information from WGIN 2003- 2008

- Link to old website on the Homepage
- Specific cross links to results, newsletters etc.

Welcome to WGIN 2nd Phase (2009-2013)

Defra Wheat Genetic Improvement Network - Improving the environmental footprint of farming through crop genetics and targeted traits analysis

Background

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Recent Updates

[RECENT UPDATES](#)

[OLD Site](#) - The old site is still available here.

Old Website

site guide

The site is grouped into the following four sections:

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About Section

Essential Information on WGIN and links to related projects

The image shows a screenshot of the WGIN website. At the top, there is a navigation bar with links for 'home', 'site map', and 'contact us'. Below this is a header section featuring the Defra logo (Department for Environment, Food and Rural Affairs), the WGIN logo in large orange letters, the Monogram logo, and the Wheat Genetic Improvement Network logo. A main navigation menu is displayed below the header, with categories: ABOUT, INFORMATION, RESOURCES, and STAKEHOLDERS. Under the 'ABOUT' category, there are several sub-links: Project Outline, Contacts, News and Events, Participants, Related Projects, WGIN Newsletter, Website Updates, and Other Defra Genetic Improvement Networks. The background of the website features a close-up image of wheat stalks.

home | site map | contact us

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WGIN

monogram

Wheat
Genetic
Improvement
Network

	ABOUT	INFORMATION	RESOURCES	STAKEHOLDERS
HOM	Project Outline			
	Contacts			
Pa	News and Events			
	Participants			
The	Related Projects			
The	WGIN Newsletter			
and	Website Updates			
reso	Other Defra Genetic Improvement Networks			

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s to receive funds are Rothamsted Research, The John Innes Centre and the University of Nottingham. The
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edge expertise in the genetic analysis of crop traits and the research groups led by Professor John Snape
ment of Crop Genetics specialise in the analysis of key wheat traits and in the provision of cutting each
at. Rothamsted Research has acknowledged expertise in the analysis of multiple crop traits using both
environment facilities. There is over 150 years experience in exploring the nitrogen requirement of the
of analysing the soil-base fungal disease called take-all, over 30 years experience in investigating wheat
experience in analysis Septoria tritici leaf blotch disease of wheat. Those currently actively engaged in
its underpinned by crop genetics are Professor Peter Shewry, Dr Malcolm Hawkesford, Professor Kim
Hammond-Kosack, Mr Richard Gutteridge and Dr Hai-Chun Jing. The University of Nottingham has acknowledged expertise in the analysis of

Information Section

Detailed information on all activities



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[home](#) | [site map](#) | [contact us](#)

WGIN



monogram



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Improvement
Network

ABOUT

INFORMATION

RESOURCES

STAKEHOLDERS

HOME >

Outline

Objective 3

Project Outline

The Avalon x Cadenza map

At JIC, the Avalon x Cadenza population was developed in response to a request to ensure that at the start of all wheat breeding programmes, there is a high level of genetic diversity. Within the funded WGIN traits research project, we have developed a take-all inoculum in a 1st wheat site in 2008. This will be used in two projects.

In addition to the original 203 A x C D mapping population, a new mapping population will become available by mid 2009 and will initially be in short supply and so will be used in a mapping population.

Summary table of Objective 3:

Target start date	Target end date	Duration in month	Objective number / description of milestone
01/12/2008	30/11/2013	60	Objective 3.1 Continue the main

[Research Objectives ...](#)

Outline

Management and Networking

2 - Near Isogenic Lines (JIC)

Meetings

3 - Avalon x Cadenza Mapping Population (JIC)

Collaborations

4 - Paragon Gamma and EMS mutagenised Lines (JIC)

Subcontractor Projects

5 - AE Watkins and Gediflux Germplasm Collections (JIC)

General Links

6 - New Mapping Populations (JIC)

Presentations

7 - Insect Resistance - Cereal Aphids (RRes)

Publications

8 - Nitrogen Use Efficiency Improvement and QTLs (RRes)

Publicity

9 - Water Use Efficiency and drought tolerance (UNo and JIC)

Reports

10 - Take All disease (RRes)

11 - Introgression of Disease Resistance (RRes)

11 - Introgression of Disease Resistance (RRes)

12 - Soil based Traits (UNo and RRes)

12 - Soil based Traits (UNo and RRes)

GANTT chart:

Month	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58
Objective 3.1																																																										

Resources Section

Research results, datasets, experimental tools and germplasm resources

The screenshot shows the WGIN website interface. At the top, there are navigation links for 'home', 'site map', and 'contact us'. The 'defra' logo is on the left, and the 'Wheat Genetic Improvement Network' logo is on the right. The main navigation bar has four tabs: 'ABOUT', 'INFORMATION', 'RESOURCES', and 'STAKEHOLDERS'. The 'RESOURCES' tab is active, showing a vertical menu with items: 'Outline', 'Germplasm', 'Molecular Markers', 'Mapping Populations' (highlighted), 'Research Results', 'Traits', 'Technical Links (Global)', and 'Glossary'. The 'STAKEHOLDERS' tab shows 'T. monococcum' and 'Hexaploid wheat'. The main content area features a heading 'Hexaploid Wheat Mapping Popula...', followed by 'Resources from WGIN 2003 - 2009:' and 'Peer reviewed publication:'. Two publications are listed with their authors and titles. A 'Dataset:' section at the bottom provides a link to 'Mapping data for the Avalon x Cadenza double haploid population'.

home | site map | contact us

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Genetic
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ABOUT INFORMATION RESOURCES STAKEHOLDERS

HOME >

Hexaploid Wheat Mapping Popula

Resources from WGIN 2003 - 2009:

Peer reviewed publication:

Al-Kaff N, Knight E, Bertin I, Foote T, Hart N, Griffiths S and Moore G. Deletion of the Ph1 locus in wheat *Triticum aestivum*: with deletion mutants and expression profiling

Hayden MJ, Stephenson P, Logojan AM, Khatkar D, Rogers C, Elsden J, Koebner RMD, Snape JW and Sharp PJ. Development and genetic mapping of sequence tagged microsatellites (STMs) in bread wheat (*Triticum aestivum* L). *Theoretical and Applied Genetics* 113 (2006), pp. 1271-1281.

Dataset:

[Mapping data for the Avalon x Cadenza double haploid population](#)

Outline
Germplasm
Molecular Markers
Mapping Populations
Research Results
Traits
Technical Links (Global)
Glossary

T. monococcum
Hexaploid wheat

mal region containing the Ph1 locus in
63-872

Stakeholder Section



[home](#) | [site map](#) | [contact us](#)

WGIN



[ABOUT](#)

[INFORMATION](#)

[RESOURCES](#)

[STAKEHOLDERS](#)

[Outline](#)

[Contacts](#)

[Meetings](#)

[Newsletters](#)

[HOME >](#)

Meetings

Future meetings:

The next stakeholder meeting will take place on the 25 November 2009 at Rothamsted Research.

Past meetings

Information on stakeholder meetings from WGIN 2003 - 2008 can be accessed on the [old website](#).

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Related Projects

About section



[home](#) | [site map](#) | [contact us](#)



ABOUT

INFORMATION

RESOURCES

STAKEHOLDERS

[HOME](#) >

Related Projects

Several [LINK Wheat Projects](#) use WGIN data in their research or cover related research topics.

Monogram: Monogram is a BBSRC funded project for the co-ordination of UK grass and cereal research. The website gives in-depth information on UK grass and cereal research, covering research projects, events and networking activities, vacancies and a host of resources for researchers.

BBSRC Crop Science Initiative: [Wheat Projects](#) You can search the BBSRC project database on <http://www.bbsrc.ac.uk/science/grants/> for full details on each project.

Wheat Genome Sequencing Projects

[International Wheat Genome Sequencing Consortium](#)
[UK Wheat Genome Project](#)

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Research Objectives

Information section



The header features the Defra logo (Department for Environment, Food and Rural Affairs) on the left, a navigation menu with 'home', 'site map', and 'contact us' in the center, and the 'monogram' and 'Wheat Genetic Improvement Network' logos on the right. The main title 'WGIN' is prominently displayed in large orange letters over a background image of wheat stalks. Below the title is a horizontal navigation bar with four orange buttons: 'ABOUT', 'INFORMATION', 'RESOURCES', and 'STAKEHOLDERS'.

HOME >

Objective 3

The Avalon x Cadenza mapping population

At JIC, the Avalon x Cadenza population seed stocks will be maintained. These stocks will be made available to other researchers upon request to ensure that at the start of all new projects the seed is multiple up from the authentic source.

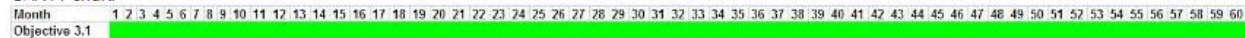
Within the funded WGIN traits research the A x C DH mapping will be used to explore differences in NUE (Objective 8) and accumulation in soil of take-all inoculum in a 1st wheat situation (Objective 10). Data generated in WGIN 1 already indicated the A x C DH is highly suitable for these two projects.

In addition to the original 203 A x C DH generated at JIC, already further DH lines are being created at RRes using core funds. These lines will become available by mid 2009 and will probably increase the size of the mapping population to over 850 lines. Seed for these DH additional will initially be in short supply and so these lines will in the first instance be used to further fine map QTLs already identified using the original mapping population.

Summary table of Objective 3:

Target start date	Target end date	Duration in month	Objective number / description of milestone
01/12/2008	30/11/2013	60	Objective 3.1 Continue the maintenance and availability of authentic seed stocks of the Avalon x Cadenza population

GANTT chart:



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Management Meetings

Information section



home | site map | contact us

ABOUT INFORMATION RESOURCES STAKEHOLDERS

HOME >

Meetings

Future Meetings

Next management meeting: 25 June 2009 at NIAB
Next stakeholder meeting: 25 November 2009 at Rothamsted Research

Past Meetings

Management Meetings

Management Meeting 12th March 2009:
[Agenda](#)
[Presentations](#)

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Technical Links



[home](#) | [site map](#) | [contact us](#)

[ABOUT](#)

[INFORMATION](#)

[RESOURCES](#)

[STAKEHOLDERS](#)

[HOME](#) >

Technical Links

This section lists links to genomics databases and websites with useful technical information on bioinformatics and cereal genetics.

Wheat Coordinated Agricultural Project (Wheat CAP): <http://maswheat.ucdavis.edu/> US project with the main goal of increasing the competitiveness of public wheat breeding programs through the intensive use of modern selection technologies, mainly Marker Assisted Selection (MAS). In this website you will find a link to a Protocols section (<http://maswheat.ucdavis.edu/protocols/index.htm>) This section has links to available MAS methods for markers for 38 different traits, including quality traits and insect, fungi and virus resistance.

Haplotype Polymorphism in Polyploid Wheats and their Diploid Ancestors: <http://probes.pw.usda.gov:8080/snpworld/Search> Project on the discovery and mapping of single nucleotide polymorphisms in tetraploid and hexaploid wheat. This project performed SNP discovery using ESTs that had been previously mapped to chromosome bins. Intron SNPs were targeted by designing genome specific primers for the A, B and D genomes. The SNP discovery panel included diploid, tetraploid, and hexaploid wheat lines. The search function allows the user to identify SNP markers for a specific chromosome or bin. The information includes the relevant genome specific primer pairs for each mapped EST and the sequence polymorphism found among the diverse wheat panel examined. An example of the use of these markers can be found in: Chao et al (2009) Analysis of gene-derived SNP marker polymorphism in US wheat cultivars. Molecular Breeding, 23:23-33 <http://www.springerlink.com/content/cj81vt2gk568523h/>

JIC Genetic Stocks: www.jic.ac.uk/GERMPLAS/Index.htm

Wheat ESTs at CerealsDB: www.cerealsdb.uk.net

JIC Gait Genotyping Data: <http://jii05.jic.bbsrc.ac.uk/Gait.html>

Molecular markers learning modules by Cornell University: <http://www.igd.cornell.edu/Training&Education.html>

Small Grains Cereal - news, resources and funding opportunities for SGC researchers: <http://www.smallgraincereals.org/>
European Triticeae Genomics Initiative (ETGI): <http://pgrc.ipk-gatersleben.de/etgi/>

CR-EST: The IPK Crop EST Database: <http://pgrc.ipk-gatersleben.de/cr-est/index.php>

Codons Optimised to Discover Deleterious Lesions (CODDLE): <http://www.proweb.org/coddle/>

GrainGenes: A USDA sponsored database for *Triticeae* and *Avena* <http://wheat.pw.usda.gov/GG2/index.shtml/>

Subcontractor Projects

Current location:

http://www.wgin.org.uk/WGIN_2/information/subcontractorprojects.php



The screenshot shows the WGIN website interface. At the top, there are navigation links for 'home', 'site map', and 'contact us'. The main header features the 'defra' logo (Department for Environment, Food and Rural Affairs), the 'WGIN' logo, the 'monogram' logo, and the 'Wheat Genetic Improvement Network' logo. Below the header is a navigation bar with four tabs: 'ABOUT', 'INFORMATION', 'RESOURCES', and 'STAKEHOLDERS'. The 'ABOUT' tab is currently selected, and a 'HOME >' link is visible below it. The main content area is titled 'Subcontractor Projects' and contains the following text:

Procurement of additional wheat research activities within the lifetime of the project:

A total sum of £50K has been set aside for two main purposes. Firstly, to enhance the value of the main projects by involving other parties that will provide novel technology or novel phenotyping expertise on related traits, for example root structure. Secondly, these funds could be used to extend promising results arising from finishing LINK projects that will benefit their commercial exploitation by the UK wheat breeders or ideas resulting from discussions with the breeders. The money will be spent either on one single project or on several smaller projects. A specific protocol will be used based on one previously successfully applied in the BBSRC funded small grain cereal project to ensure the allocation of these funds is done in a fair and unbiased manner. This will involve a short written application in a specific format, peer review by a set panel of experts, and a final vote by a small committee especially selected for this purpose by the WGIN management team.

If you are interested in bidding for a subcontractor project please fill in the application form below.

Application form for subcontractor projects:

Application form for subcontractor projects:

Name:

Organisation:

Address:

Email:

Short CV:

Background proposed project: (max. 500 words)

Brief workplan: (max. 1000 words)

Relevance to WGIN objectives: (max. 500 words)

From:

To:

Estimated Costs:

Salaries:

Other expenses:

VAT:

Total:

Subcontractor Projects

Required application details:

- Name
- Organisation
- Address
- E-Mail
- Short CV:
- Background of proposed project
- Brief Workplan
- Relevance of WGIN objectives
- Start and finish date
- Estimated cost (Breakdown in salaries, other expenses and VAT)

Keeping the website up to date requires ongoing input of researchers

- New and updated datasets
and any other results
- Outreach activities
- Any publications
- Useful links

Please send any information on the
above to elke.anzinger@bbsrc.ac.uk or
to wgin.defra@bbsrc.ac.uk

Feedback and Suggestions

If you have feedback on the website
please send it to
elke.anzinger@bbsrc.ac.uk

A big thanks to Pierre Carrion who provided the design for the new WGIN website.